Errors Corrected by the STIC Systems Branch

Batch #5

Serial Number: 09/183,672A

ENTERED

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: _____
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____.
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: _____
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: _____
- ☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____.
- ☐ Inserted mandatory headings, specifically: _____
- ☐ Corrected an obvious error in the response, specifically: _____
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: _____
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- ☑ Other: Corrected misaligned amino acid numbering. Seqs. 378, 525.

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95

1644

RAW SEQUENCE LISTING DATE: 09/11/2000
PATENT APPLICATION: US/09/483,672A TIME: 10:24:17

Input Set : A:\Pto.amc
Output Set: N:\CRF3\09112000\I483672A.raw

See p. 5

3 <110> APPLICANT: Xu, Jiangchun
4 Dillon, Davin C.
5 Mitcham, Jennifer L.
6 Harlocker, Susan Louise
7 Jiang Yuqui
8 Reed, Steven G.
9 Kalos, Michael D.
10 Fanger, Gary R.
11 Retter, Marc W.
12 Solk, John A.
13 Day, Craig H.
14 Skeiky, Yasir A.W.
15 Wang, Aijun
16 Meagher, Madeleine

18 <120> TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
19 DIAGNOSIS OF PROSTATE CANCER
21 <130> FILE REFERENCE: 210121.42711C11
C--> 23 **<140> CURRENT APPLICATION NUMBER: US/09/483,672A**
24 <141> CURRENT FILING DATE: 2000-01-14
26 <160> NUMBER OF SEQ ID NOS: 590
28 <170> SOFTWARE: FastSEQ for Windows Version 3.0
30 <210> SEQ ID NO: 1
31 <211> LENGTH: 814
32 <212> TYPE: DNA
33 <213> ORGANISM: Homo sapien
35 <220> FEATURE:
36 <221> NAME/KEY: misc_feature
37 <222> LOCATION: (1)...(814)
38 <223> OTHER INFORMATION: n = A,T,C or G
40 <400> SEQUENCE: 1
41 ttttttttt tttttcacag tataacagct ctttatttct gtgagttcta ctaggaaatc 60
42 atcaaatctg agggttgtct ggaggacttc aatacacctc cccccatagt gaatcagctt 120
43 ccaggggtc cagtccctct ccttacttca tccccatccc atgccaaagg aagaccctcc 180
44 ctccttggct cacagccttc tctaggcttc ccagtgcctc caggacagag tgggttatgt 240
45 tttcagctcc atccttgctg tgagtgtctg gtgcgttgtg cctccagctt ctgctcagtg 300
46 cttcatggac agtgtccagc acatgtcact ctccactctc tcagtgtgga tccactagtt 360
47 ctagagcggc cgccaccgcg gtggagctcc agcttttgtt ccctttagtg agggttaatt 420
48 gcgcgcttgg cgtaatcatg gtcataactg tttcctgtgt gaaattgtta tccgctcaca 480
49 attccacaca acatacgagc cggaagcata aagtgtaaag cctggggtgc ctaatgagtg 540
W--> 50 **anctaactca cattaattgc gttgcgctca ctgnccgctt tccagtcngg aaaactgtcg 600**
W--> 51 **tgccagctgc attaatgaat cggccaacgc ncggggaaaa gcggtttgcg ttttgggggc 660**
W--> 52 **tcttccgctt ctcgctcact nantcctgcg ctcggtcntt cggctgcggg gaacggtatc 720**
W--> 53 **actcctcaaa ggnggtatta cggttatccn naaatcnggg gatacccngg aaaaaanttt 780**
W--> 54 **aacaaaaggg cancaaaggg cngaaacgta aaaa** 814
56 <210> SEQ ID NO: 2
57 <211> LENGTH: 816
58 <212> TYPE: DNA

RAW SEQUENCE LISTING DATE: 09/11/2000
PATENT APPLICATION: US/09/483,672A TIME: 10:24:17

Input Set : A:\Pto.amc
Output Set: N:\CRF3\09112000\I483672A.raw

59 <213> ORGANISM: Homo sapien
61 <220> FEATURE:
62 <221> NAME/KEY: misc_feature
63 <222> LOCATION: (1)...(816)
64 <223> OTHER INFORMATION: n = A,T,C or G
66 <400> SEQUENCE: 2
67 acagaaatgt tggatggtgg agcacctttc tatacgactt acaggacagc agatggggaa 60
68 ttcatggctg ttggagcaat agaaccccag ttctacgagc tgctgatcaa aggacttgga 120
69 ctaaagtctg atgaacttcc caatcagatg agcatggatg attggccaga aatgaagaag 180
70 aagtttgcag atgtatttgc aaagaagacg aaggcagagt ggtgtcaaat ctttgacggc 240
71 acagatgcct gtgtgactcc ggttctgact tttgaggagg ttgttcatca tgatcacaac 300
72 aaggaacggg gctcgtttat caccagtgag gagcaggacg tgagcccccg ccctgcacct 360
73 ctgctgttaa acaccccagc catcccttct ttcaaaaggg atccactagt tctagaagcg 420
74 gccgccaccg cggtggagct ccagcttttg ttccctttag tgagggttaa ttgcgcgctt 480
75 ggcgtaatca tggtcatagc tgtttcctgt gtgaaattgt tatccgctca caattccccc 540
W--> 76 aacatacgag ccggaacata aagtgttaag cctggggtgc ctaatgantg agctaactcn 600
W--> 77 cattaattgc gttgcgctca ctgcccgctt tccagtcggg aaaactgtcg tgccactgcn 660
W--> 78 ttantgaatc ngccaccccc cgggaaaagg cggttgcntt ttgggcctct tccgctttcc 720
W--> 79 tcgctcattg atcctngcnc ccggtcttcg gctgcggnga acggttcact cctcaaaggc 780
W--> 80 ggtntnccgg ttatccccaa acnggggata cccnga 816
82 <210> SEQ ID NO: 3
83 <211> LENGTH: 773
84 <212> TYPE: DNA
85 <213> ORGANISM: Homo sapien
87 <220> FEATURE:
88 <221> NAME/KEY: misc_feature
89 <222> LOCATION: (1)...(773)
90 <223> OTHER INFORMATION: n = A,T,C or G
92 <400> SEQUENCE: 3
93 cttttgaaag aagggatggc tggggtgttt aacagcagag gtgcagggcg ggggctcacg 60
94 tcctgctcct cactggtgat aaacgagccc cgttccttgt tgtgatcatg atgaacaacc 120
95 tcctcaaaag tcagaaccgg agtcacacag gcatctgtgc cgtcaaagat ttgacaccac 180
96 tctgccttcg tcttctttgc aaatacatct gcaaacttct tcttcatttc tggccaatca 240
W--> 97 tccatgctca tctgattggg aagttcatca gactttagtc canntccttt gatcagcagc 300
98 tcgtagaact ggggttctat tgctccaaca gccatgaatt ccccatctgc tgtcctgtaa 360
99 gtcgtataga aaggtgctcc accatccaac atgttctgtc ctcgaggggg ggcccggtac 420
W--> 100 ccaattcgcc ctatantgag tcgtattacg cgcgctcact ggccgtcgtt ttacaacgtc 480
101 gtgactggga aaaccctggg cgttaccaac ttaatcgcct tgcagcacat ccccctttcg 540
W--> 102 ccagctgggc gtaatancga aaaggcccgc accgatcgcc cttccaacag ttgcgcacct 600
W--> 103 gaatgggnaa atgggacccc cctgttaccg cgcattnaac ccccgcnggg tttngttgtt 660
W--> 104 acccccacnt nnaccgctta cactttgcca gcgccttanc gcccgctccc tttcnccttt 720
W--> 105 cttcccttcc tttcncnccn ctttcccccg gggtttcccc cntcaaaccc cna 773
107 <210> SEQ ID NO: 4
108 <211> LENGTH: 828
109 <212> TYPE: DNA
110 <213> ORGANISM: Homo sapien
112 <220> FEATURE:
113 <221> NAME/KEY: misc_feature
114 <222> LOCATION: (1)...(828)

RAW SEQUENCE LISTING DATE: 09/11/2000
PATENT APPLICATION: US/09/483,672A TIME: 10:24:17

Input Set : A:\Pto.amc
Output Set: N:\CRF3\09112000\I483672A.raw

115 <223> OTHER INFORMATION: n = A,T,C or G
117 <400> SEQUENCE: 4
118 cctcctgagt cctactgacc tgtgctttct ggtgtggagt ccagggctgc taggaaaagg 60
119 aatgggcaga cacaggtgta tgccaatgtt tctgaaatgg gtataatttc gtcctctcct 120
120 tcggaacact ggctgtctct gaagacttct cgctcagttt cagtgaggac acacacaaag 180
121 acgtgggtga ccatgttgtt tgtggggtgc agagatggga ggggtggggc ccaccctgga 240
122 agagtggaca gtgacacaag gtggacactc tctacagatc actgaggata agctggagcc 300
W--> 123 acaatgcatg aggcacacac acagcaagga tgacnctgta aacatagccc acgctgtcct 360
W--> 124 gnggggcactg ggaagcctan atnaggccgt gagcanaaag aaggggagga tccactagtt 420
W--> 125 ctanagcggc cgccaccgcg gtgganctcc anctttgttt ccctttagtg agggttaatt 480
W--> 126 gcgcgcttgg cntaatcatg gtcatanctn tttcctgtgt gaaattgtta tccgctcaca 540
W--> 127 attccacaca acatacganc cggaaacata aantgtaaac ctggggtgcc taatgantga 600
W--> 128 ctaactcaca ttaattgcgt tgcgctcact gcccgctttc caatcnggaa acctgtcttg 660
W--> 129 ccncttgcat tnatgaatcn gccaaccccc ggggaaaagc gtttgcgttt tgggcgctct 720
W--> 130 tccgcttcct cnctcantta ntccctncnc tcggtcattc cggctgcngc aaaccggttc 780
W--> 131 accncctcca aagggggtat tccggtttcc ccnaatccgg gganancc 828
133 <210> SEQ ID NO: 5
134 <211> LENGTH: 834
135 <212> TYPE: DNA
136 <213> ORGANISM: Homo sapien
138 <220> FEATURE:
139 <221> NAME/KEY: misc_feature
140 <222> LOCATION: (1)...(834)
141 <223> OTHER INFORMATION: n = A,T,C or G
143 <400> SEQUENCE: 5
144 ttttttttt tttttactga tagatggaat ttattaagct tttcacatgt gatagcacat 60
145 agttttaatt gcatccaaag tactaacaaa aactctagca atcaagaatg gcagcatgtt 120
146 attttataac aatcaacacc tgtggctttt aaaatttggt tttcataaga taatttatac 180
147 tgaagtaaat ctagccatgc ttttaaaaaa tgctttaggt cactccaagc ttggcagtta 240
148 acatttggca taaacaataa taaaacaatc acaatttaat aaataacaaa tacaacattg 300
149 taggccataa tcatatacag tataaggaaa aggtggtagt gttgagtaag cagttattag 360
150 aatagaatac cttggcctct atgcaaatat gtctagacac tttgattcac tcagccctga 420
151 cattcagttt tcaaagtagg agacaggttc tacagtatca ttttacagtt tccaacacat 480
152 tgaaaacaag tagaaaatga tgagttgatt tttattaatg cattacatcc tcaagagtta 540
153 tcaccaaccc ctcagttata aaaaattttc aagttatatt agtcatataa cttggtgtgc 600
154 ttattttaaa ttagtgctaa atggattaag tgaagacaac aatggtcccc taatgtgatt 660
W--> 155 gatattggtc atttttacca gcttctaaat ctnaactttc aggcttttga actggaacat 720
W--> 156 tgnatnacag tgttccanag ttncaaccta ctggaacatt acagtgtgct tgattcaaaa 780
W--> 157 tgttattttg ttaaaaatta aattttaacc tggtggaaaa ataatttgaa atna 834
159 <210> SEQ ID NO: 6
160 <211> LENGTH: 818
161 <212> TYPE: DNA
162 <213> ORGANISM: Homo sapien
164 <220> FEATURE:
165 <221> NAME/KEY: misc_feature
166 <222> LOCATION: (1)...(818)
167 <223> OTHER INFORMATION: n = A,T,C or G
169 <400> SEQUENCE: 6
170 ttttttttt ttttttttt aagaccctca tcaatagatg gagacataca gaaatagtca 60

RAW SEQUENCE LISTING DATE: 09/11/2000
PATENT APPLICATION: US/09/483,672A TIME: 10:24:17

Input Set : A:\Pto.amc
Output Set: N:\CRF3\09112000\I483672A.raw

```
     171  aaccacatct acaaaatgcc agtatcaggc ggcggcttcg aagccaaagt gatgtttgga     120
     172  tgtaaagtga aatattagtt ggcggatgaa gcagatagtg aggaaagttg agccaataat     180
     173  gacgtgaagt ccgtggaagc ctgtggctac aaaaaatgtt gagccgtaga tgccgtcgga     240
     174  aatggtgaag ggagactcga agtactctga ggcttgtagg agggtaaaat agagacccag     300
     175  taaaattgta ataagcagtg cttgaattat ttggtttcgg ttgttttcta ttagactatg     360
     176  gtgagctcag gtgattgata ctcctgatgc gagtaatacg gatgtgttta ggagtgggac     420
     177  ttctagggga tttagcgggg tgatgcctgt tgggggccag tgccctccta gttggggggt     480
     178  aggggctagg ctggagtggt aaaaggctca gaaaaatcct gcgaagaaaa aaacttctga     540
     179  ggtaataaat aggattatcc cgtatcgaag gccttttgg acaggtggtg tgtggtggcc     600
     180  ttggtatgtg ctttctcgtg ttacatcgcg ccatcattgg tatatggtta gtgtgttggg     660
W--> 181  ttantanggc ctantatgaa gaacttttgg antggaatta aatcaatngc ttggccggaa     720
W--> 182  gtcattanga nggctnaaaa ggccctgtta ngggtctggg ctnggtttta cccnacccat     780
W--> 183  ggaatncncc ccccggacna ntgnatccct attcttaa                           818
     185 <210> SEQ ID NO: 7
     186 <211> LENGTH: 817
     187 <212> TYPE: DNA
     188 <213> ORGANISM: Homo sapien
     190 <220> FEATURE:
     191 <221> NAME/KEY: misc_feature
     192 <222> LOCATION: (1)...(817)
     193 <223> OTHER INFORMATION: n = A,T,C or G
     195 <400> SEQUENCE: 7
     196  ttttttttt ttttttttt tggctctaga gggggtagag ggggtgctat agggtaaata      60
     197  cgggccctat ttcaaagatt tttaggggaa ttaattctag gacgatgggt atgaaactgt     120
     198  ggtttgctcc acagatttca gagcattgac cgtagtatac ccccggtcgt gtagcggtga     180
     199  aagtggtttg gtttagacgt ccgggaattg catctgtttt taagcctaat gtggggacag     240
W--> 200  ctcatgagtg caagacgtct tgtgatgtaa ttattatacn aatgggggct tcaatcggga     300
     201  gtactactcg attgtcaacg tcaaggagtc gcaggtcgcc tggttctagg aataatgggg     360
     202  gaagtatgta ggaattgaag attaatccgc cgtagtcggt gttctcctag gttcaatacc     420
     203  attggtggcc aattgatttg atggtaaggg gagggatcgt tgaactcgtc tgttatgtaa     480
W--> 204  aggatncctt ngggatggga aggcnatnaa ggactangga tnaatggcgg gcangatatt     540
W--> 205  tcaaacngtc tctanttcct gaaacgtctg aaatgttaat aanaattaan tttngttatt     600
W--> 206  gaatnttnng gaaaagggct tacaggacta gaaaccaaat angaaaanta atnntaangg     660
W--> 207  cnttatcntn aaaggtnata accnctccta tnatcccacc caatngnatt ccccacncnn     720
W--> 208  acnattggat nccccanttc canaaanggc cnccccccgg tgnannccnc cttttgttcc     780
W--> 209  cttnantgan ggttattcnc ccctngcntt atcancc                            817
     211 <210> SEQ ID NO: 8
     212 <211> LENGTH: 799
     213 <212> TYPE: DNA
     214 <213> ORGANISM: Homo sapien
     216 <220> FEATURE:
     217 <221> NAME/KEY: misc_feature
     218 <222> LOCATION: (1)...(799)
     219 <223> OTHER INFORMATION: n = A,T,C or G
     221 <400> SEQUENCE: 8
     222  catttccggg tttactttct aaggaaagcc gagcggaagc tgctaacgtg ggaatcggtg      60
     223  cataaggaga actttctgct ggcacgcgct agggacaagc gggagagcga ctccgagcgt     120
     224  ctgaagcgca cgtcccagaa ggtggacttg gcactgaaac agctgggaca catccgcgag     180
     225  tacgaacagc gcctgaaagt gctggagcgg gaggtccagc agtgtagccg cgtcctgggg     240
```

RAW SEQUENCE LISTING DATE: 09/11/2000
PATENT APPLICATION: US/09/483,672A TIME: 10:24:17

Input Set : A:\Pto.amc
Output Set: N:\CRF3\09112000\I483672A.raw

```
W--> 226  tgggtggccg angcctganc cgctctgcct tgctgccccc angtgggccg ccaccccctg     300
W--> 227  acctgcctgg gtccaaacac tgagccctgc tggcggactt caagganaac ccccacangg     360
W--> 228  ggattttgct cctanantaa ggctcatctg ggcctcggcc cccccacctg gttggccttg     420
W--> 229  tctttgangt gagccccatg tccatctggg ccactgtcng gaccaccttt ngggagtgtt     480
W--> 230  ctccttacaa ccacannatg cccggctcct cccggaaacc antcccancc tgngaaggat     540
W--> 231  caagncctgn atccactnnt nctanaaccg gccnccnccg cngtggaacc cnccttntgt     600
W--> 232  tccttttcnt tnagggttaa tnncgccttg gccttnccan ngtcctncnc nttttccnnt     660
W--> 233  gttnaaattg ttangcnccc nccnntcccn cnncnncnan cccgacccnn annttnnann     720
W--> 234  ncctgggggt nccnncngat tgacccnncc nccctntant tgcnttnggg nncnntgccc     780
W--> 235  ctttccctct ngggganncg                                               799
      237 <210> SEQ ID NO: 9
      238 <211> LENGTH: 801
      239 <212> TYPE: DNA
      240 <213> ORGANISM: Homo sapien
      242 <220> FEATURE:
      243 <221> NAME/KEY: misc_feature
      244 <222> LOCATION: (1)...(801)
      245 <223> OTHER INFORMATION: n = A,T,C or G
      247 <400> SEQUENCE: 9
      248  acgccttgat cctcccaggc tgggactggt tctgggagga gccgggcatg ctgtggtttg      60
W--> 249  taangatgac actcccaaag gtggtcctga cagtggccca gatggacatg gggctcacct     120
      250  caaggacaag gccaccaggt gcgggggccg aagcccacat gatccttact ctatgagcaa     180
W--> 251  aatcccctgt gggggcttct ccttgaagtc cgccancagg gctcagtctt tggacccang     240
W--> 252  caggtcatgg ggttgtngnc caactggggg ccncaacgca aaanggcnca gggcctcngn     300
W--> 253  cacccatccc angacgcggc tacactnctg gacctcccnc tccaccactt tcatgcgctg     360
W--> 254  ttcntacccg cgnatntgtc ccanctgttt cngtgccnac tccancttct nggacgtgcg     420
W--> 255  ctacatacgc ccggantcnc nctcccgctt tgtccctatc cacgtnccan caacaaattt     480
W--> 256  cnccntantg caccnattcc cacntttnnc agntttccnc nncgngcttc cttntaaaag     540
W--> 257  ggttganccc cggaaaatnc cccaaagggg gggggccngg tacccaactn ccccctnata     600
W--> 258  gctgaantcc ccatnaccnn gnctcnatgg ancentccnt tttaannacn ttctnaactt     660
W--> 259  gggaanancc ctcgnccntn cccccnttaa tcccnccttg cnangnncnt cccccnntcc     720
W--> 260  ncccnnntng gcntntnann cnaaaaaggc ccnnnancaa tctcctnncn cctcanttcg     780
W--> 261  ccancctcg aaatcggccn c                                              801
      263 <210> SEQ ID NO: 10
      264 <211> LENGTH: 789
      265 <212> TYPE: DNA
      266 <213> ORGANISM: Homo sapien
      268 <220> FEATURE:
      269 <221> NAME/KEY: misc_feature
      270 <222> LOCATION: (1)...(789)
      271 <223> OTHER INFORMATION: n = A,T,C or G
      273 <400> SEQUENCE: 10
W--> 274  cagtctatnt ggccagtgtg gcagctttcc ctgtggctgc cggtgccaca tgcctgtccc      60
      275  acagtgtggc cgtggtgaca gcttcagccg ccctcaccgg gttcaccttc tcagccctgc     120
      276  agatcctgcc ctacacactg gcctccctct accaccggga gaagcaggtg ttcctgccca     180
      277  aataccgagg ggacactgga ggtgctagca gtgaggacag cctgatgacc agcttcctgc     240
      278  caggccctaa gcctggagct cccttcccta atggacacgt gggtgctgga ggcagtggcc     300
      279  tgctcccacc tccacccgcg ctctgcgggg cctctgcctg tgatgtctcc gtacgtgtgg     360
W--> 280  tggtgggtga gcccaccgan gccagggtgg ttccgggccg gggcatctgc ctggacctcg     420
```

F.Y.I.

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY DATE: 09/11/2000
PATENT APPLICATION: US/09/483,672A TIME: 10:24:18

Input Set : A:\Pto.amc
Output Set: N:\CRF3\09112000\I483672A.raw

L:23 M:270 C: Current Application Number differs, Wrong Format
L:50 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:51 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:52 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:53 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:54 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:76 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:77 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:78 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:79 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:80 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:97 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:100 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:102 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:103 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:104 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:105 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:123 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:124 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:125 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:126 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:127 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:128 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:129 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:130 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:131 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:155 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:156 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:157 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:181 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:182 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:183 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:200 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:204 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:205 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:206 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:207 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:208 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:209 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:226 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:227 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:228 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:229 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:230 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:231 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:232 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:233 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:234 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8

VERIFICATION SUMMARY DATE: 09/11/2000
PATENT APPLICATION: US/09/483,672A TIME: 10:24:18

Input Set : A:\Pto.amc
Output Set: N:\CRF3\09112000\I483672A.raw

L:235 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:249 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:251 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:698 M:283 W: Missing Blank Line separator, <210> field identifier
L:1467 M:283 W: Missing Blank Line separator, <400> field identifier
L:10018 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:502
L:10018 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:502
L:10018 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:502
L:10018 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:502
L:10018 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:502
L:10019 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:502
L:10019 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:502
L:10019 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:502
L:10019 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:502
M:340 Repeated in SeqNo=502
L:10020 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:502
L:10020 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:502
L:10020 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:502
L:10020 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:502
L:10021 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:502
L:10021 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:502
L:10021 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:502
L:10021 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:502
L:10023 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:502
L:10023 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:502
L:10023 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:502
L:10023 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:502
L:10031 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:503
L:10031 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:503
L:10031 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:503
L:10031 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:503
L:10031 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:503
L:10032 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:503
L:10032 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:503
L:10032 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:503
L:10032 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:503
M:340 Repeated in SeqNo=503
L:10033 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:503
L:10033 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:503
L:10033 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:503
L:10033 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:503
L:10035 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:503
L:10035 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:503
L:10035 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:503
L:10035 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:503
L:10036 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:503
L:10036 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:503
L:10036 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:503
L:10036 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:503

VERIFICATION SUMMARY DATE: 09/11/2000
PATENT APPLICATION: US/09/483,672A TIME: 10:24:18

Input Set : A:\Pto.amc
Output Set: N:\CRF3\09112000\I483672A.raw

L:10037 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:503
L:10037 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:503
L:10037 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:503
L:10037 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:503
L:10107 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:508
L:10107 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:508
L:10107 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:508
L:10107 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:508
L:10107 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:508

1644

RAW SEQUENCE LISTING DATE: 09/11/2000
PATENT APPLICATION: US/09/483,672A TIME: 15:29:37

Input Set : A:\42711c11.app
Output Set: N:\CRF3\09112000\I483672A.raw

Does Not Comply
Corrected Diskette Needed

These errors have been edited

```
  3 <110> APPLICANT: Xu, Jiangchun
  4       Dillon, Davin C.
  5       Mitcham, Jennifer L.
  6       Harlocker, Susan Louise
  7       Jiang Yuqui
  8       Reed, Steven G.
  9       Kalos, Michael D.
 10       Fanger, Gary R.
 11       Retter, Marc W.
 12       Solk, John A.
 13       Day, Craig H.
 14       Skeiky, Yasir A.W.
 15       Wang, Aijun
 16       Meagher, Madeleine
 18 <120> TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
 19       DIAGNOSIS OF PROSTATE CANCER
 21 <130> FILE REFERENCE: 210121.42711C11
C--> 23 <140> CURRENT APPLICATION NUMBER: US/09/483,672A
 24 <141> CURRENT FILING DATE: 2000-01-14
 26 <160> NUMBER OF SEQ ID NOS: 590
 28 <170> SOFTWARE: FastSEQ for Windows Version 3.0
```

ERRORED SEQUENCES

```
7200 <210> SEQ ID NO: 378
7201 <211> LENGTH: 1719
7202 <212> TYPE: PRT
7203 <213> ORGANISM: Homo sapien
7205 <400> SEQUENCE: 378
7206  Met Val Val Glu Val Asp Ser Met Pro Ala Ala Ser Ser Val Lys Lys
7207   1               5                  10                  15
7208  Pro Phe Gly Leu Arg Ser Lys Met Gly Lys Trp Cys Cys Arg Cys Phe
7209              20                  25                  30
7210  Pro Cys Cys Arg Glu Ser Gly Lys Ser Asn Val Gly Thr Ser Gly Asp
7211          35                  40                  45
7212  His Asp Asp Ser Ala Met Lys Thr Leu Arg Ser Lys Met Gly Lys Trp
7213      50                  55                  60
7214  Cys Arg His Cys Phe Pro Cys Cys Arg Gly Ser Gly Lys Ser Asn Val
7215  65                  70                  75                  80
7216  Gly Ala Ser Gly Asp His Asp Asp Ser Ala Met Lys Thr Leu Arg Asn
7217                  85                  90                  95
7218  Lys Met Gly Lys Trp Cys Cys His Cys Phe Pro Cys Cys Arg Gly Ser
7219              100                 105                 110
7220  Gly Lys Ser Lys Val Gly Ala Trp Gly Asp Tyr Asp Asp Ser Ala Phe
7221          115                 120                 125
7222  Met Glu Pro Arg Tyr His Val Arg Gly Glu Asp Leu Asp Lys Leu His
```

RAW SEQUENCE LISTING DATE: 09/11/2000
PATENT APPLICATION: US/09/483,672A TIME: 15:29:38

Input Set : A:\42711c11.app
Output Set: N:\CRF3\09112000\I483672A.raw

```
7223      130                 135                 140
7224  Arg Ala Ala Trp Trp Gly Lys Val Pro Arg Lys Asp Leu Ile Val Met
7225  145                 150                 155                 160
7226  Leu Arg Asp Thr Asp Val Asn Lys Lys Asp Lys Gln Lys Arg Thr Ala
7227                  165                 170                 175
7228  Leu His Leu Ala Ser Ala Asn Gly Asn Ser Glu Val Val Lys Leu Leu
7229              180                 185                 190
7230  Leu Asp Arg Arg Cys Gln Leu Asn Val Leu Asp Asn Lys Lys Arg Thr
7231          195                 200                 205
7232  Ala Leu Ile Lys Ala Val Gln Cys Gln Glu Asp Glu Cys Ala Leu Met
7233      210                 215                 220
7234  Leu Leu Glu His Gly Thr Asp Pro Asn Ile Pro Asp Glu Tyr Gly Asn
7235  225                 230                 235                 240
7236  Thr Thr Leu His Tyr Ala Ile Tyr Asn Glu Asp Lys Leu Met Ala Lys
7237                  245                 250                 255
7238  Ala Leu Leu Leu Tyr Gly Ala Asp Ile Glu Ser Lys Asn Lys His Gly
7239              260                 265                 270
7240  Leu Thr Pro Leu Leu Leu Gly Val His Glu Gln Lys Gln Gln Val Val
7241          275                 280                 285
7242  Lys Phe Leu Ile Lys Lys Lys Ala Asn Leu Asn Ala Leu Asp Arg Tyr
7243      290                 295                 300
7244  Gly Arg Thr Ala Leu Ile Leu Ala Val Cys Cys Gly Ser Ala Ser Ile
7245  305                 310                 315                 320
7246  Val Ser Leu Leu Leu Glu Gln Asn Ile Asp Val Ser Ser Gln Asp Leu
7247                  325                 330                 335
7248  Ser Gly Gln Thr Ala Arg Glu Tyr Ala Val Ser Ser His His His Val
7249              340                 345                 350
7250  Ile Cys Gln Leu Leu Ser Asp Tyr Lys Glu Lys Gln Met Leu Lys Ile
7251          355                 360                 365
7252  Ser Ser Glu Asn Ser Asn Pro Glu Asn Val Ser Arg Thr Arg Asn Lys
7253      370                 375                 380
7254  Pro Arg Thr His Met Val Val Glu Val Asp Ser Met Pro Ala Ala Ser
7255  385                 390                 395                 400
7256  Ser Val Lys Lys Pro Phe Gly Leu Arg Ser Lys Met Gly Lys Trp Cys
7257                  405                 410                 415
7258  Cys Arg Cys Phe Pro Cys Cys Arg Glu Ser Gly Lys Ser Asn Val Gly
7259              420                 425                 430
7260  Thr Ser Gly Asp His Asp Asp Ser Ala Met Lys Thr Leu Arg Ser Lys
7261          435                 440                 445
7262  Met Gly Lys Trp Cys Arg His Cys Phe Pro Cys Cys Arg Gly Ser Gly
7263      450                 455                 460
7264  Lys Ser Asn Val Gly Ala Ser Gly Asp His Asp Asp Ser Ala Met Lys
7265  465                 470                 475                 480
7266  Thr Leu Arg Asn Lys Met Gly Lys Trp Cys Cys His Cys Phe Pro Cys
7267                  485                 490                 495
7268  Cys Arg Gly Ser Gly Lys Ser Lys Val Gly Ala Trp Gly Asp Tyr Asp
7269              500                 505                 510
7270  Asp Ser Ala Phe Met Glu Pro Arg Tyr His Val Arg Gly Glu Asp Leu
7271          515                 520                 525
```

RAW SEQUENCE LISTING DATE: 09/11/2000
PATENT APPLICATION: US/09/483,672A TIME: 15:29:38

Input Set : A:\4271lc11.app
Output Set: N:\CRF3\09112000\I483672A.raw

```
7272  Asp Lys Leu His Arg Ala Ala Trp Trp Gly Lys Val Pro Arg Lys Asp
7273      530                 535                 540
7274  Leu Ile Val Met Leu Arg Asp Thr Asp Val Asn Lys Lys Asp Lys Gln
7275  545                 550                 555                 560
7276  Lys Arg Thr Ala Leu His Leu Ala Ser Ala Asn Gly Asn Ser Glu Val
7277                  565                 570                 575
7278  Val Lys Leu Leu Leu Asp Arg Arg Cys Gln Leu Asn Val Leu Asp Asn
7279              580                 585                 590
7280  Lys Lys Arg Thr Ala Leu Ile Lys Ala Val Gln Cys Gln Glu Asp Glu
7281          595                 600                 605
7282  Cys Ala Leu Met Leu Leu Glu His Gly Thr Asp Pro Asn Ile Pro Asp
7283      610                 615                 620
7284  Glu Tyr Gly Asn Thr Thr Leu His Tyr Ala Ile Tyr Asn Glu Asp Lys
7285  625                 630                 635                 640
7286  Leu Met Ala Lys Ala Leu Leu Leu Tyr Gly Ala Asp Ile Glu Ser Lys
7287                  645                 650                 655
7288  Asn Lys His Gly Leu Thr Pro Leu Leu Leu Gly Val His Glu Gln Lys
7289              660                 665                 670
7290  Gln Gln Val Val Lys Phe Leu Ile Lys Lys Lys Ala Asn Leu Asn Ala
7291          675                 680                 685
7292  Leu Asp Arg Tyr Gly Arg Thr Ala Leu Ile Leu Ala Val Cys Cys Gly
7293      690                 695                 700
7294  Ser Ala Ser Ile Val Ser Leu Leu Leu Glu Gln Asn Ile Asp Val Ser
7295  705                 710                 715                 720
7296  Ser Gln Asp Leu Ser Gly Gln Thr Ala Arg Glu Tyr Ala Val Ser Ser
7297                  725                 730                 735
7298  His His His Val Ile Cys Gln Leu Leu Ser Asp Tyr Lys Glu Lys Gln
7299              740                 745                 750
7300  Met Leu Lys Ile Ser Ser Glu Asn Ser Asn Pro Glu Gln Asp Leu Lys
7301          755                 760                 765
7302  Leu Thr Ser Glu Glu Glu Ser Gln Arg Phe Lys Gly Ser Glu Asn Ser
7303      770                 775                 780
7304  Gln Pro Glu Lys Met Ser Gln Glu Pro Glu Ile Asn Lys Asp Gly Asp
7305  785                 790                 795                 800
7306  Arg Glu Val Glu Glu Glu Met Lys Lys His Glu Ser Asn Asn Val Gly
7307                  805                 810                 815
7308  Leu Leu Glu Asn Leu Thr Asn Gly Val Thr Ala Gly Asn Gly Asp Asn
7309              820                 825                 830
7310  Gly Leu Ile Pro Gln Arg Lys Ser Arg Thr Pro Glu Asn Gln Gln Phe
7311          835                 840                 845
7312  Pro Asp Asn Glu Ser Glu Glu Tyr His Arg Ile Cys Glu Leu Val Ser
7313      850                 855                 860
7314  Asp Tyr Lys Glu Lys Gln Met Pro Lys Tyr Ser Ser Glu Asn Ser Asn
7315  865                 870                 875                 880
7316  Pro Glu Gln Asp Leu Lys Leu Thr Ser Glu Glu Glu Ser Gln Arg Leu
7317                  885                 890                 895
7318  Glu Gly Ser Glu Asn Gly Gln Pro Glu Leu Glu Asn Phe Met Ala Ile
7319              900                 905                 910
7320  Glu Glu Met Lys Lys His Gly Ser Thr His Val Gly Phe Pro Glu Asn
```

RAW SEQUENCE LISTING DATE: 09/11/2000
PATENT APPLICATION: US/09/483,672A TIME: 15:29:38

Input Set : A:\4271lc11.app
Output Set: N:\CRF3\09112000\I483672A.raw

```
     7321          915                 920                 925
     7322  Leu Thr Asn Gly Ala Thr Ala Gly Asn Gly Asp Asp Gly Leu Ile Pro
     7323      930                 935                 940
     7324  Pro Arg Lys Ser Arg Thr Pro Glu Ser Gln Gln Phe Pro Asp Thr Glu
     7325  945                 950                 955                 960
     7326  Asn Glu Glu Tyr His Ser Asp Glu Gln Asn Asp Thr Gln Lys Gln Phe
     7327                  965                 970                 975
     7328  Cys Glu Glu Gln Asn Thr Gly Ile Leu His Asp Glu Ile Leu Ile His
     7329              980                 985                 990
     7330  Glu Glu Lys Gln Ile Glu Val Val Glu Lys Met Asn Ser Glu Leu Ser
     7331          995                 1000                1005
     7332  Leu Ser Cys Lys Lys Glu Lys Asp Ile Leu His Glu Asn Ser Thr Leu
     7333      1010                1015                1020
     7334  Arg Glu Glu Ile Ala Met Leu Arg Leu Glu Leu Asp Thr Met Lys His
E--> 7335  1025                1030                1035                104
     7336  Gln Ser Gln Leu Pro Arg Thr His Met Val Val Glu Val Asp Ser Met
     7337                  1045                1050                1055
     7338  Pro Ala Ala Ser Ser Val Lys Lys Pro Phe Gly Leu Arg Ser Lys Met
     7339              1060                1065                1070
     7340  Gly Lys Trp Cys Cys Arg Cys Phe Pro Cys Cys Arg Glu Ser Gly Lys
     7341          1075                1080                1085
     7342  Ser Asn Val Gly Thr Ser Gly Asp His Asp Asp Ser Ala Met Lys Thr
     7343      1090                1095                1100
     7344  Leu Arg Ser Lys Met Gly Lys Trp Cys Arg His Cys Phe Pro Cys Cys
E--> 7345  1105                1110                1115                112
     7346  Arg Gly Ser Gly Lys Ser Asn Val Gly Ala Ser Gly Asp His Asp Asp
     7347                  1125                1130                1135
     7348  Ser Ala Met Lys Thr Leu Arg Asn Lys Met Gly Lys Trp Cys Cys His
     7349              1140                1145                1150
     7350  Cys Phe Pro Cys Cys Arg Gly Ser Gly Lys Ser Lys Val Gly Ala Trp
     7351          1155                1160                1165
     7352  Gly Asp Tyr Asp Asp Ser Ala Phe Met Glu Pro Arg Tyr His Val Arg
     7353      1170                1175                1180
     7354  Gly Glu Asp Leu Asp Lys Leu His Arg Ala Ala Trp Trp Gly Lys Val
E--> 7355  1185                1190                1195                120
     7356  Pro Arg Lys Asp Leu Ile Val Met Leu Arg Asp Thr Asp Val Asn Lys
     7357                  1205                1210                1215
     7358  Lys Asp Lys Gln Lys Arg Thr Ala Leu His Leu Ala Ser Ala Asn Gly
     7359              1220                1225                1230
     7360  Asn Ser Glu Val Val Lys Leu Leu Leu Asp Arg Arg Cys Gln Leu Asn
     7361          1235                1240                1245
     7362  Val Leu Asp Asn Lys Lys Arg Thr Ala Leu Ile Lys Ala Val Gln Cys
     7363      1250                1255                1260
     7364  Gln Glu Asp Glu Cys Ala Leu Met Leu Leu Glu His Gly Thr Asp Pro
E--> 7365  1265                1270                1275                128
     7366  Asn Ile Pro Asp Glu Tyr Gly Asn Thr Thr Leu His Tyr Ala Ile Tyr
     7367                  1285                1290                1295
     7368  Asn Glu Asp Lys Leu Met Ala Lys Ala Leu Leu Leu Tyr Gly Ala Asp
     7369              1300                1305                1310
```

Invalid Amino Acid Numbering.

Right side:

His 1040
His → 104

Cys 1120
Cys → 112

Val 1200
Val → 120

Pro 1280
Pro → 128

RAW SEQUENCE LISTING DATE: 09/11/2000
PATENT APPLICATION: US/09/483,672A TIME: 15:29:38

Input Set : A:\42711c11.app
Output Set: N:\CRF3\09112000\I483672A.raw

```
     7370  Ile Glu Ser Lys Asn Lys His Gly Leu Thr Pro Leu Leu Leu Gly Val
     7371          1315                1320                1325
     7372  His Glu Gln Lys Gln Gln Val Val Lys Phe Leu Ile Lys Lys Lys Ala
     7373      1330                1335                1340
     7374  Asn Leu Asn Ala Leu Asp Arg Tyr Gly Arg Thr Ala Leu Ile Leu Ala
E--> 7375  1345                1350                1355                136
     7376  Val Cys Cys Gly Ser Ala Ser Ile Val Ser Leu Leu Leu Glu Gln Asn
     7377                1365                1370                1375
     7378  Ile Asp Val Ser Ser Gln Asp Leu Ser Gly Gln Thr Ala Arg Glu Tyr
     7379            1380                1385                1390
     7380  Ala Val Ser Ser His His His Val Ile Cys Gln Leu Leu Ser Asp Tyr
     7381          1395                1400                1405
     7382  Lys Glu Lys Gln Met Leu Lys Ile Ser Ser Glu Asn Ser Asn Pro Glu
     7383      1410                1415                1420
     7384  Gln Asp Leu Lys Leu Thr Ser Glu Glu Glu Ser Gln Arg Phe Lys Gly
E--> 7385  1425                1430                1435                144
     7386  Ser Glu Asn Ser Gln Pro Glu Lys Met Ser Gln Glu Pro Glu Ile Asn
     7387                1445                1450                1455
     7388  Lys Asp Gly Asp Arg Glu Val Glu Glu Glu Met Lys Lys His Glu Ser
     7389            1460                1465                1470
     7390  Asn Asn Val Gly Leu Leu Glu Asn Leu Thr Asn Gly Val Thr Ala Gly
     7391          1475                1480                1485
     7392  Asn Gly Asp Asn Gly Leu Ile Pro Gln Arg Lys Ser Arg Thr Pro Glu
     7393      1490                1495                1500
     7394  Asn Gln Gln Phe Pro Asp Asn Glu Ser Glu Glu Tyr His Arg Ile Cys
E--> 7395  1505                1510                1515                152
     7396  Glu Leu Val Ser Asp Tyr Lys Glu Lys Gln Met Pro Lys Tyr Ser Ser
     7397                1525                1530                1535
     7398  Glu Asn Ser Asn Pro Glu Gln Asp Leu Lys Leu Thr Ser Glu Glu Glu
     7399            1540                1545                1550
     7400  Ser Gln Arg Leu Glu Gly Ser Glu Asn Gly Gln Pro Glu Lys Arg Ser
     7401          1555                1560                1565
     7402  Gln Glu Pro Glu Ile Asn Lys Asp Gly Asp Arg Glu Leu Glu Asn Phe
     7403      1570                1575                1580
     7404  Met Ala Ile Glu Glu Met Lys Lys His Gly Ser Thr His Val Gly Phe
E--> 7405  1585                1590                1595                160
     7406  Pro Glu Asn Leu Thr Asn Gly Ala Thr Ala Gly Asn Gly Asp Asp Gly
     7407                1605                1610                1615
     7408  Leu Ile Pro Pro Arg Lys Ser Arg Thr Pro Glu Ser Gln Gln Phe Pro
     7409            1620                1625                1630
     7410  Asp Thr Glu Asn Glu Glu Tyr His Ser Asp Glu Gln Asn Asp Thr Gln
     7411          1635                1640                1645
     7412  Lys Gln Phe Cys Glu Glu Gln Asn Thr Gly Ile Leu His Asp Glu Ile
     7413      1650                1655                1660
     7414  Leu Ile His Glu Glu Lys Gln Ile Glu Val Val Glu Lys Met Asn Ser
E--> 7415  1665                1670                1675                168
     7416  Glu Leu Ser Leu Ser Cys Lys Lys Glu Lys Asp Ile Leu His Glu Asn
     7417                1685                1690                1695
     7418  Ser Thr Leu Arg Glu Glu Ile Ala Met Leu Arg Leu Glu Leu Asp Thr
```

Same as previous page

RAW SEQUENCE LISTING DATE: 09/11/2000
PATENT APPLICATION: US/09/483,672A TIME: 15:29:38

Input Set : A:\42711c11.app
Output Set: N:\CRF3\09112000\I483672A.raw

```
7419              1700                1705                1710
7420  Met Lys His Gln Ser Gln Leu
7421          1715
10356 <210> SEQ ID NO: 525
10357 <211> LENGTH: 254
10358 <212> TYPE: PRT
10359 <213> ORGANISM: Homo sapien
10361 <400> SEQUENCE: 525
10362 Met Ala Thr Ala Gly Asn Pro Trp Gly Trp Phe Leu Gly Tyr Leu Ile
10363  1               5                  10                  15
10364 Leu Gly Val Ala Gly Ser Leu Val Ser Gly Ser Cys Ser Gln Ile Ile
10365              20                  25                  30
10366 Asn Gly Glu Asp Cys Ser Pro His Ser Gln Pro Trp Gln Ala Ala Leu
10367          35                  40                  45
10368 Val Met Glu Asn Glu Leu Phe Cys Ser Gly Val Leu Val His Pro Gln
10369      50                  55                  60
10370 Trp Val Leu Ser Ala Ala His Cys Phe Gln Asn Ser Tyr Thr Ile Gly
10371 65                  70                  75                  80
10372 Leu Gly Leu His Ser Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met
10373                  85                  90                  95
10374 Val Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro Leu
10375              100                 105                 110
10376 Leu Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu
10377          115                 120                 125
10378 Ser Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala
10379      130                 135                 140
10380 Gly Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly Arg
10381 145                 150                 155                 160
10382 Met Pro Thr Val Leu Gln Cys Val Asn Val Ser Val Val Ser Glu Glu
10383                  165                 170                 175
10384 Val Cys Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe Cys
10385              180                 185                 190
10386 Ala Gly Gly Gly Gln Asp Gln Lys Asp Ser Cys Asn Gly Asp Ser Gly
10387          195                 200                 205
10388 Gly Pro Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe Gly
10389      210                 215                 220
10390 Lys Ala Pro Cys Gly Gln Val Gly Val Pro Gly Val Tyr Thr Asn Leu
10391 225                 230                 235                 240
10392 Cys Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Ala Ser
E--> 10393 245 250 ------> 250
```

Invalid amino acid numbering

VERIFICATION SUMMARY DATE: 09/11/2000
PATENT APPLICATION: US/09/483,672A TIME: 15:29:40

Input Set : A:\42711c11.app
Output Set: N:\CRF3\09112000\I483672A.raw

L:23 M:270 C: Current Application Number differs, Wrong Format
L:50 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:51 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:52 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:53 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:54 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:76 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:77 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:78 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:79 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:80 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:97 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:100 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:102 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:103 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:104 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:105 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:123 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:124 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:125 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:126 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:127 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:128 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:129 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:130 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:131 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:155 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:156 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:157 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:181 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:182 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:183 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:200 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:204 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:205 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:206 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:207 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:208 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:209 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:226 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:227 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:228 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:229 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:230 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:231 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:232 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:233 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:234 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8

VERIFICATION SUMMARY DATE: 09/11/2000
PATENT APPLICATION: US/09/483,672A TIME: 15:29:40

Input Set : A:\42711c11.app
Output Set: N:\CRF3\09112000\I483672A.raw

L:235 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:249 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:251 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:698 M:283 W: Missing Blank Line separator, <210> field identifier
L:1467 M:283 W: Missing Blank Line separator, <400> field identifier
L:7335 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:378
M:332 Repeated in SeqNo=378
L:10018 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:502
L:10018 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:502
L:10018 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:502
L:10018 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:502
L:10018 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:502
L:10019 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:502
L:10019 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:502
L:10019 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:502
L:10019 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:502
M:340 Repeated in SeqNo=502
L:10020 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:502
L:10020 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:502
L:10020 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:502
L:10020 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:502
L:10021 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:502
L:10021 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:502
L:10021 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:502
L:10021 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:502
L:10023 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:502
L:10023 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:502
L:10023 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:502
L:10023 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:502
L:10031 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:503
L:10031 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:503
L:10031 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:503
L:10031 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:503
L:10031 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:503
L:10032 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:503
L:10032 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:503
L:10032 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:503
L:10032 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:503
M:340 Repeated in SeqNo=503
L:10033 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:503
L:10033 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:503
L:10033 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:503
L:10033 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:503
L:10035 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:503
L:10035 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:503
L:10035 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:503
L:10035 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:503
L:10036 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:503
L:10036 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:503

VERIFICATION SUMMARY DATE: 09/11/2000
PATENT APPLICATION: US/09/483,672A TIME: 15:29:40

Input Set : A:\42711c11.app
Output Set: N:\CRF3\09112000\I483672A.raw

L:10036 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:503
L:10036 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:503
L:10037 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:503
L:10037 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:503
L:10037 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:503
L:10037 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:503
L:10107 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:508
L:10107 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:508
L:10107 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:508
L:10107 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:508
L:10107 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:508
L:10393 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:525